

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 7, 2005, 06:56:21 ; Search time 75.9095 Seconds
(without alignments)
1349.183 Million cell updates/sec

Title: US-09-939-537-31_COPY_1_200
Perfect score: 1029
Sequence: 1 NMRGVPFRHLVLVQLALP.....TWTCVLQNKVKEFRIDIV 200

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 1023 | 99.4 | 458 | 1 | CD4_HUMAN |
| 2 | 999 | 97.1 | 458 | 1 | CD4_PANTR |
| 3 | 912 | 88.6 | 458 | 1 | CD4_MACP |
| 4 | 910 | 88.4 | 458 | 1 | CD4_MACP |
| 5 | 904 | 87.9 | 458 | 1 | CD4_MACP |
| 6 | 903 | 87.8 | 458 | 1 | CD4_MACP |
| 7 | 885 | 86.0 | 458 | 1 | CD4_CERAB |
| 8 | 784 | 76.2 | 397 | 1 | CD4_CERAB |
| 9 | 783 | 76.1 | 397 | 1 | CD4_CERAB |
| 10 | 767 | 74.5 | 397 | 2 | 009261 |
| 11 | 767 | 74.5 | 397 | 2 | 009262 |
| 12 | 767 | 74.5 | 397 | 2 | 009263 |
| 13 | 767 | 74.5 | 397 | 2 | 009264 |
| 14 | 763 | 74.1 | 397 | 2 | 009265 |
| 15 | 763 | 74.1 | 397 | 2 | 009266 |
| 16 | 741.5 | 72.1 | 457 | 2 | 08H2T8 |
| 17 | 740.5 | 72.0 | 457 | 2 | 08H2T7 |
| 18 | 737.5 | 71.7 | 457 | 1 | CD4_SAIISC |
| 19 | 598 | 58.1 | 453 | 1 | CD4_CANPA |
| 20 | 597 | 58.0 | 455 | 2 | 0710E2 |
| 21 | 592 | 57.5 | 455 | 2 | 09X8T8 |
| 22 | 587.5 | 57.1 | 459 | 1 | CD4_RABIT |
| 23 | 562 | 54.6 | 432 | 2 | 06LBR1 |
| 24 | 557.5 | 54.2 | 474 | 2 | P79355 |
| 25 | 553 | 53.7 | 457 | 2 | 06GYR3 |
| 26 | 531 | 51.6 | 406 | 2 | 06GRN3 |
| 27 | 531 | 51.6 | 447 | 2 | 06GRN4 |
| 28 | 488.5 | 47.5 | 457 | 1 | CD4_RAT |
| 29 | 467 | 45.4 | 457 | 1 | CD4_MOUSE |
| 30 | 467 | 45.4 | 457 | 2 | 061396 |
| 31 | 436.5 | 42.4 | 433 | 2 | 055054 |

| | | | | | | |
|----|-------|------|-----|---|--------|--------------------|
| 32 | 400 | 38.9 | 86 | 2 | 077596 | 077596 mandrillus |
| 33 | 400 | 38.9 | 86 | 2 | 077597 | 077597 mandrillus |
| 34 | 397 | 38.6 | 86 | 2 | 077594 | 077594 cercopithec |
| 35 | 397 | 38.6 | 86 | 2 | 077599 | 077599 theropithec |
| 36 | 395 | 38.4 | 86 | 2 | 077595 | 077595 cercocobus |
| 37 | 395 | 38.4 | 86 | 2 | 077595 | 077595 cercocobus |
| 38 | 392 | 38.1 | 86 | 2 | 077598 | 077598 papio sp. (|
| 39 | 388 | 37.7 | 86 | 2 | 077601 | 077601 lophocobus |
| 40 | 383 | 37.2 | 86 | 2 | 077600 | 077600 lophocobus |
| 41 | 380 | 36.9 | 78 | 2 | 06LCP8 | 06LCP8 homo sapien |
| 42 | 357 | 34.7 | 71 | 2 | 013969 | 013969 homo sapien |
| 43 | 305.5 | 29.7 | 99 | 2 | 029027 | 029027 sus scrofa |
| 44 | 280.5 | 27.3 | 99 | 2 | 029028 | 029028 sus scrofa |
| 45 | 172 | 16.7 | 482 | 2 | 090WB5 | 090WB5 anas platyr |

ALIGNMENTS

RESULT 1
CD4_HUMAN
ID CD4_HUMAN STANDARD; PRT; 458 AA.
AC P01730;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE T-cell surface glycoprotein CD4 precursor (T-cell surface antigen
DE T4/Leu-3).
GN Name=CD4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85254948; PubMed=2990730;
RA Maddon P.J., Littman D.R., Godfrey M., Maddon D.E., Chese L., Axel R.;
RT "The isolation and nucleotide sequence of a cDNA encoding the T cell
RT surface protein T4: a new member of the immunoglobulin gene family.";
RL Cell 42:93-104(1985).
RN [2]
RP REVISION TO 26.
RX MEDLINE=89028665; PubMed=3263213; DOI=10.1016/0092-8674(88)90211-5;
RA Littman D.R., Maddon P.J., Axel R.;
RT "Corrected CD4 sequence.";
RL Cell 55:541-541(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96303695; PubMed=8723724;
RA Anasari-Lari M.A., Muzny D.M., Lu J., Lu F., Lilley C.E., Spanos S.,
RA Malley T., Gibbs R.A.;
RT "A gene-rich cluster between the CD4 and triosephosphate isomerase
RT genes at human chromosome 12p13.";
RL Genome Res. 6:314-326(1996).
RN [4]
RP SEQUENCE FROM N.A. AND VARIANT TRP-265.
RX MEDLINE=91216786; PubMed=1708753; DOI=10.1016/0198-8859(91)90077-M;
RA Hodge T.W., Sasso D.R., McDougal J.S.;
RT "Humans with OKT4-epitope deficiency have a single nucleotide base
RT change in the CD4 gene, resulting in substitution of TRP240 for
RT ARG240.";
RL Hum. Immunol. 30:99-104(1991).
RN [5]
RP SEQUENCE FROM N.A.
RX TISSUE=Pancreas;
RC MEDLINE=23888257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Krausberg R.L., Reingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schlier G.D.,
RA Altschul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsien L.,
RA Diaktenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Tohiyuki S., Carninci P., Prange C.,

RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunatille P.H.,
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
RA Villalón D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettunen M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shechenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.B.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.",
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RN SEQUENCE OF 28-424 FROM N.A.
RP TISSUE=Blood;
RC MEDLINE=93049640; PubMed=1425921;
RX Fomsgaard A., Hirsch V.M., Johnson P.R.,
RT "Cloning and sequences of primate CD4 molecules: diversity of the
RT cellular receptor for simian immunodeficiency virus/human
RT immunodeficiency virus.",
RT Eur. J. Immunol. 22:2973-2981(1992).
RN [7]
RN SEQUENCE OF 26-394, AND DISULFIDE BOND.
RX MEDLINE=90078232; PubMed=2592374;
RA Carr S.A., Hemling M.E., Polena-Waserman G., Sweet R.W., Anumula K.,
RA Barr J.R., Huddleston M.J., Taylor P.,
RT "Protein and carbohydrate structural analysis of a recombinant soluble
RT CD4 receptor by mass spectrometry.",
RT J. Biol. Chem. 264:21286-21295(1989).
RN [8]
RN SEQUENCE OF 26-40.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.,
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.",
RT Protein Sci. 13:2819-2824(2004).
RN [9]
RN REMOVAL FROM CELL SURFACE BY HIV-1 NEF, AND MUTAGENESIS OF MET-432;
RX SER-433; 438-LEU-LEU-439 AND SER-440.
RX PubMed=8124721;
RA "Nef induces CD4 endocytosis: requirement for a critical dileucine
RT motif in the membrane-proximal CD4 cytoplasmic domain.",
RT Cell 76:853-864(1994).
RN [10]
RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 26-208.
RX MEDLINE=91061801; PubMed=1701030; DOI=10.1038/348411a0;
RA Wang J., Yan Y., Garrett T.P., Liu J., Rodgers D.W., Garlick R.L.,
RA Tarr G.E., Husain Y., Reinherz E.L., Harrison S.C.,
RT "Atomic structure of a fragment of human CD4 containing two
RT immunoglobulin-like domains.",
RT Nature 348:411-416(1990).
RN [11]
RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 26-208.
RX MEDLINE=91061882; PubMed=22471146; DOI=10.1038/348419a0;
RA Ryu S.-E., Kwong P.D., Truneh A., Porter T.G., Arthos J.,
RA Rosenberg M., Dai X., Xuong N.-H., Axel R., Sweet R.W.,
RA Hendrickson W.A.,
RT "Crystal structure of an HIV-binding recombinant fragment of human
RT CD4.",
RT Nature 348:419-426(1990).
RN [12]
RN X-RAY CRYSTALLOGRAPHY (3.9 ANGSTROMS) OF 26-388.
RX MEDLINE=97311402; PubMed=9168119;
RA Wu H., Kwong P.D., Hendrickson W.A.,
RT "Dimeric association and segmental variability in the structure of
RT human CD4.",
RT Nature 387:527-530(1997).
RN [13]
RN PALMITOYLATION.
RX MEDLINE=92317088; PubMed=1618861;
RA Cripe B., Rose J.K.,

RT "Identification of palmitoylation sites on CD4, the human
RT immunodeficiency virus receptor.",
RT J. Biol. Chem. 267:13593-13597(1992).
RL -1- FUNCTION: Accessory protein for MHC class-II antigen/T-cell
CC interaction. May regulate T-cell activation.
CC -1- SUBUNIT: Associates with p56-lck.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Removed from plasma
CC membrane by HIV-1 Nef protein that increases clathrin-dependent
CC endocytosis of this antigen to target it to lysosomal degradation.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD4 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd4.htm".
CC -----
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CC -----
CC EMBL; M12807; AAA3572.1; -;
CC EMBL; U47924; AA51309.1; -;
CC EMBL; M35160; AAA16069.1; -;
CC EMBL; BC025782; AAH25782.1; -;
CC PIR; A90872; RMHTY4.
CC PDB; 1CDH; X-ray; @=26-203.
CC PDB; 1CDI; X-ray; @=25-203.
CC PDB; 1CDJ; X-ray; @=26-203.
CC PDB; 1CDU; X-ray; @=26-203.
CC PDB; 1CDV; X-ray; @=26-203.
CC PDB; 1GDM; X-ray; C=26-210.
CC PDB; 1G9N; X-ray; C=26-210.
CC PDB; 1GCI; X-ray; C=26-210.
CC PDB; 1UT4; X-ray; C=26-203.
CC PDB; 1Q68; NMR; A=421-458.
CC PDB; 1WER; NMR; A=427-445.
CC PDB; 1WTO; X-ray; A/B=26-388.
CC PDB; 1WIP; X-ray; A/B=26-388.
CC PDB; 1WIO; X-ray; A/B=26-388.
CC PDB; 3CD4; X-ray; @=26-207.
CC GlycoSuiteDB; P01730; -;
CC Genew; HGNC:1678; CD4.
CC H-InvDB; HIX0023001; -;
CC MIM; 186940; -;
CC GO; GO:0005886; C:plasma membrane; TAS.
CC GO; GO:0042101; C:T-cell receptor complex; NMS.
CC GO; GO:0015026; F:coreceptor activity; TAS.
CC GO; GO:0015029; F:internalization receptor activity; TAS.
CC GO; GO:0042289; F:MHC class II protein binding; NMS.
CC GO; GO:0004888; F:transmembrane receptor activity; TAS.
CC GO; GO:0006955; P:immune response; NMS.
CC GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . .; NMS.
CC GO; GO:0030217; P:T-cell differentiation; NMS.
CC GO; GO:0045058; P:T-cell selection; NMS.
CC GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; NMS.
CC InterPro; IPR008424; CD2.
CC InterPro; IPR000973; CD4_TCSG.
CC InterPro; IPR007110; IG_Like.
CC InterPro; IPR003596; IG_V.
CC Pfam; PF00047; Ig_2.
CC PRINTS; PR00692; CD4TCANTIGEN.
CC SMART; SMO0406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
CC 3D-structure; Direct protein sequencing; Glycoprotein;
CC Immune response; Immunoglobulin domain; Lipoprotein; Palmitate;
CC Polymorphism; Repeat; Signal; T-cell; Transmembrane.
CC SIGNAL; 1; 25
CC CHAIN; 26; 458 T-cell surface glycoprotein CD4.
CC DOMAIN; 26; 396 Extracellular (Potential).
CC TRANSMEM; 397; 418 Potential.
CC DOMAIN; 419; 458 Cytoplasmic (Potential).
CC FT

FT DOMAIN 26 125 Ig-like V-type.
 FT DOMAIN 126 203 Ig-like C2-type 1.
 Query Match 99.4%; Score 1023; DB 1; Length 458;
 Best Local Similarity 99.5%; Pred. No. 3.5e-77;
 Matches 199; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLVLTQALPAATQGNKVVYGGKGDVETCTASQKSIQPHKNSNQK 60
 DB 1 MNRGVPFRHLVLTQALPAATQGNKVVYGGKGDVETCTASQKSIQPHKNSNQK 60
 QY 61 IIGNGSFLTKGSPSKLNDRASSRLMDQGNFPLIIKNIKIEDSDTYICEVEDQKEVOL 120
 DB 61 IIGNGSFLTKGSPSKLNDRASSRLMDQGNFPLIIKNIKIEDSDTYICEVEDQKEVOL 120
 QY 121 LVFGLTANSDTHLLOQOSLTLTLESPGSSPVQCSPPKKNIOGKKTLSVSQLDQSG 180
 DB 121 LVFGLTANSDTHLLOQOSLTLTLESPGSSPVQCSPPKKNIOGKKTLSVSQLDQSG 180
 QY 181 TWTCVTLQNGKVEFKIDIV 200
 DB 181 TWTCVTLQNGKVEFKIDIV 200

RESULT 2
 CD4_PANTR STANDARD; PRT; 458 AA.
 AC P16T04;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE T-cell surface glycoprotein CD4 precursor (T-cell surface antigen T4/Leu-3).
 DE Name=CD4;
 OS Pan troglodytes (chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.
 NCBI_TaxId=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90182664; PubMed=2107024; DOI=10.1016/0092-8674(90)90089-W;
 RA Camerini D., Seed B.;
 RT "A CD4 domain important for HIV-mediated syncytium formation lies outside the virus binding site.";
 RL Cell 60:747-754(1990).
 RN [2]
 RP SEQUENCE OF 26-424 FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=93049640; PubMed=1425921;
 RA Fomsgaard A., Hirsch V.M., Johnson P.R.;
 RT "Cloning and sequences of primate CD4 molecules: diversity of the cellular receptor for simian immunodeficiency virus/human immunodeficiency virus.";
 RL Eur. J. Immunol. 22:2973-2981(1992).
 CC -1- FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.
 CC -1- SUBUNIT: Associates with p56-lck (by similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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 CC
 DR EMBL: M31135; AAA35407.1; -;
 DR EMBL: X73323; CAAS1749.1; -;
 DR PIR: B32722; RWCZ74.
 DR HSSP: P01730; 1W1Q.

DR GO:0042101; C:T-cell receptor complex, ISS.
 DR GO:0015026; P:coreceptor activity, ISS.
 DR GO:0042289; P:MHC class II protein binding, ISS.
 DR GO:0006955; P:immune response, ISS.
 DR GO:0045086; P:positive regulation of interleukin-2 biosyn. . .; ISS.
 DR GO:00030217; P:T-cell differentiation, ISS.
 DR GO:0045058; P:T-cell selection, ISS.
 DR GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; ISS.
 DR InterPro: IPR008424; CD2.
 DR InterPro: IPR000973; CD4_TcAg.
 DR InterPro: IPR007110; Ig-Like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig_2.
 DR PRINTS: PR00692; CD4TCANTIGEN.
 DR SMART: SM00406; IGV_1.
 DR PROSITE: PS00835; IG_LIKE_1.
 KW Glycoprotein; Immune response; Immunoglobulin domain; Lipoprotein; K W Palmate; Repeat; Signal; T-cell; Transmembrane.
 FT SIGNAL 1 25
 FT CHAIN 26 458
 FT DOMAIN 26 396
 FT TRANSMEM 397 418
 FT DOMAIN 419 458
 FT DOMAIN 26 125
 FT DOMAIN 126 203
 FT DOMAIN 204 317
 FT DOMAIN 318 374
 FT CARBOHYD 296 296
 FT CARBOHYD 325 325
 FT DISULFID 41 109
 FT DISULFID 155 184
 FT DISULFID 328 370
 FT LIPID 419 419
 FT LIPID 422 422
 FT CONFLICT 42 42
 FT CONFLICT 62 62
 FT CONFLICT 191 191
 SQ SEQUENCE 458 AA; 51057 MW; A7C3AC8A5257D3AD CRC64;

Query Match 97.1%; Score 999; DB 1; Length 458;
 Best Local Similarity 97.5%; Pred. No. 3.6e-75;
 Matches 195; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MNRGVPFRHLVLTQALPAATQGNKVVYGGKGDVETCTASQKSIQPHKNSNQK 60
 DB 1 MNRGVPFRHLVLTQALPAATQGNKVVYGGKGDVETCTASQKSIQPHKNSNQK 60
 QY 61 IIGNGSFLTKGSPSKLNDRASSRLMDQGNFPLIIKNIKIEDSDTYICEVEDQKEVOL 120
 DB 61 IIGNGSFLTKGSPSKLNDRASSRLMDQGNFPLIIKNIKIEDSDTYICEVEDQKEVOL 120
 QY 121 LVFGLTANSDTHLLOQOSLTLTLESPGSSPVQCSPPKKNIOGKKTLSVSQLDQSG 180
 DB 121 LVFGLTANSDTHLLOQOSLTLTLESPGSSPVQCSPPKKNIOGKKTLSVSQLDQSG 180
 QY 181 TWTCVTLQNGKVEFKIDIV 200
 DB 181 TWTCVTLQNGKVEFKIDIV 200

RESULT 3
 CD4_MACFA STANDARD; PRT; 458 AA.
 AC P79185;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE T-cell surface glycoprotein CD4 precursor (T-cell surface antigen T4/Leu-3).
 DE Name=CD4;
 OS Macaca fascicularis (Crab eating macaque) (Cynomolpus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;

OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9543;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymocyte;
RA Tatum M., Yabe M., Yamada Y.K.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Accessory protein for MHC class-II antigen/T-cell
CC receptor interaction. May regulate T-cell activation.
CC -1- SUBUNIT: Associates with p56-lck (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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CC -----
DR EMBL: D63349; BAA09672.1; -.
DR HSSP: P01730; 1MBR.
DR GO: GO:0042101; C: T-cell receptor complex; ISS.
DR GO: GO:0015026; F: coreceptor activity; ISS.
DR GO: GO:0042289; F: MHC class II protein binding; ISS.
DR GO: GO:0006955; P: immune response; ISS.
DR GO: GO:0045086; P: positive regulation of interleukin-2 biosyn. . .; ISS.
DR GO: GO:0030217; P: T-cell differentiation; ISS.
DR GO: GO:0045058; P: T-cell selection; ISS.
DR GO: GO:0007169; P: transmembrane receptor protein tyrosine kin. . .; ISS.
DR InterPro: IPR008424; CD2.
DR InterPro: IPR000973; CD4_TcAg.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_2.
DR PRINTS: PRO0692; CD4TCANTIGEN.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Glycoprotein; Immune response; Immunoglobulin domain; Lipoprotein;
KW Palmitate; Repeat; Signal; T-cell; Transmembrane.
FT SIGNAL 1 25
FT CHAIN 26 458
FT DOMAIN 26 396
FT TRANSMEM 397 418
FT DOMAIN 419 458
FT DOMAIN 26 125
FT DOMAIN 126 203
FT DOMAIN 204 317
FT DOMAIN 318 374
FT CARBOHYD 42 42
FT CARBOHYD 296 296
FT CARBOHYD 325 325
FT DISULFID 41 109
FT DISULFID 155 184
FT DISULFID 328 370
FT LIPID 419 419
FT LIPID 422 422
SQ SEQUENCE 458 AA; 50872 MW; 9105479F5C56FF7 CKC64;
Query Match 88.6%; Score 912; DB 1; Length 458;
Best Local Similarity 88.0%; Pred. No. 6.8e-68;
Matches 176; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

OY 121 LVFGITANSPTLHLQGGSLTTLTSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDDSG 180
DB 121 LVFGITANSPTLHLQGGSLTTLTSPGSSPSVQCRSPRGKNIQGGKTLVSQLELDDSG 180
OY 181 TWCTCTVQLQNKVEFKIDIV 200
DB 181 TWCTCTVQLQNKVEFKIDIV 200
RESULT 4
ID CD4_MACFU STANDARD; PRT; 458 AA.
AC P79184;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE T-cell surface glycoprotein CD4 precursor (T-cell surface antigen
DE T4/Leu-3).
GN Name=CD4;
OS Macaca fuscata fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9543;
RN [1]
RP SEQUENCE FROM N.A.
RA Hashimoto O., Tatum M.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Accessory protein for MHC class-II antigen/T-cell
CC receptor interaction. May regulate T-cell activation.
CC -1- SUBUNIT: Associates with p56-lck (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D63348; BAA09672.1; -.
DR HSSP: P01730; 1MBR.
DR GO: GO:0042101; C: T-cell receptor complex; ISS.
DR GO: GO:0015026; F: coreceptor activity; ISS.
DR GO: GO:0042289; F: MHC class II protein binding; ISS.
DR GO: GO:0006955; P: immune response; ISS.
DR GO: GO:0045086; P: positive regulation of interleukin-2 biosyn. . .; ISS.
DR GO: GO:0030217; P: T-cell differentiation; ISS.
DR GO: GO:0045058; P: T-cell selection; ISS.
DR GO: GO:0007169; P: transmembrane receptor protein tyrosine kin. . .; ISS.
DR InterPro: IPR008424; CD2.
DR InterPro: IPR000973; CD4_TcAg.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_2.
DR PRINTS: PRO0692; CD4TCANTIGEN.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Glycoprotein; Immune response; Immunoglobulin domain; Lipoprotein;
KW Palmitate; Repeat; Signal; T-cell; Transmembrane.
FT SIGNAL 1 25
FT CHAIN 26 458
FT DOMAIN 26 396
FT TRANSMEM 397 418
FT DOMAIN 419 458
FT DOMAIN 26 125
FT DOMAIN 126 203
FT DOMAIN 204 317
FT DOMAIN 318 374
FT CARBOHYD 42 42

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FT CARBOHYD 296 296 N-linked (GlcNAc... ) (By similarity).
FT CARBOHYD 325 325 N-linked (GlcNAc... ) (By similarity).
FT DISULFID 41 109 By similarity.
FT DISULFID 155 184 By similarity.
FT DISULFID 328 370 By similarity.
FT LIPID 419 419 S-palmitoyl cysteine (By similarity).
FT LIPID 422 422 S-palmitoyl cysteine (By similarity).
SQ SEQUENCE 458 AA; 50828 MW; 76B3E7EF08185535 CRC64;

Query Match 88.4%; Score 910; DB 1; Length 458;
Best Local Similarity 87.5%; Pred. No. 1e-67;
Matches 175; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 1 NMRGVPFRLLLVLTQALLPAATQGNKVVLTGKGGDVEITCTASQKSKIQPFHKNSNQIK 60
DB 1 NMRGVPFRLLLVLTQALLPAATQGNKVVLTGKGGDVEITCTASQKSKIQPFHKNSNQIK 60
QY 61 IIGNQSFTLKPSKLNDRADSRSLMDQGNPFLTIKLIKIEDSDTYICEVEDQKEEVL 120
DB 61 IIGNQSFTLKPSKLNDRADSRSLMDQGNPFLTIKLIKIEDSDTYICEVEDQKEEVL 120
QY 121 LVFGLTANSDFTHLQGSITLTLESPPGSSPVQCRSPKGNIOGKRTSVSOLBLQDSG 180
DB 121 LVFGLTANSDFTHLQGSITLTLESPPGSSPVQCRSPKGNIOGKRTSVSOLBLQDSG 180
QY 181 TWTCTVLONOKVKEFKIDIV 200
DB 181 TWTCTVLONOKVKEFKIDIV 200
DB 181 TWTCTVSDQKVEFKIDIV 200

RESULT 5
CD4_MACMU STANDARD; PRT; 458 AA.
ID CD4_MACMU STANDARD; PRT; 458 AA.
AC P16003; Q29617;
DT 01-APR-1990 (Rel. 14, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE T-cell surface glycoprotein CD4 precursor (T-cell surface antigen T4/Leu-3).
GN Name=CD4;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OC NCB1_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90182664; PubMed=2107024; DOI=10.1016/0092-8674(90)90089-W;
RA Camerini D., Seed B.;
RT "A CD4 domain important for HIV-mediated syncytium formation lies outside the virus binding site.";
RL Cell 60:747-754(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Thymocytes;
RA Hashimoto O., Tateuchi M.;
RT "Molecular cloning and expression of macaque CD4s.";
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 28-424 FROM N.A.
RX TISSUE=Blood;
RA Fomsgaard A., Hirsch V.M., Johnson P.R.;
RT "Cloning and sequences of primate CD4 molecules: diversity of the cellular receptor for simian immunodeficiency virus/human immunodeficiency virus.";
RL Eur. J. Immunol. 22:2973-2981(1992).
RN [4]
RP SEQUENCE OF 107-192 FROM N.A.
RX MEDLINE=98320644; PubMed=9656488;
RA Harris B.E., Disocelli T.R.;
RT "Nuclear gene trees and the phylogenetic relationships of the mangabeys (Primates: Papionini).";

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RL Mol. Biol. Evol. 15:892-900(1998).
CC -1- FUNCTION: Accessory protein for MHC class-II antigen/T-cell
CC -1- receptor interaction. May regulate T-cell activation.
CC -1- SUBUNIT: Associates with p56-lck (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M3134; AAA36838.1; -
DR EMBL; D63347; BAA09671.1; -
DR EMBL; X73326; CAA51752.1; -
DR EMBL; AF057385; AAC25129.1; -
DR HSSP; P01730; 1MR.
DR GO; GO:0042101; C: T-cell receptor complex; ISS.
DR GO; GO:0015026; F: coreceptor activity; ISS.
DR GO; GO:0042289; F: MHC class II protein binding; ISS.
DR GO; GO:0065955; P: immune response; ISS.
DR GO; GO:0045086; P: positive regulation of interleukin-2 biosyn. .; ISS.
DR GO; GO:0030217; P: T-cell differentiation; ISS.
DR GO; GO:0045058; P: T-cell selection; ISS.
DR GO; GO:0007169; P: transmembrane receptor protein tyrosine kin. .; ISS.
DR InterPro; IPR008424; CD2.
DR InterPro; IPR000973; CD4 TCAG.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_2.
DR PRINTS; PR00692; CD4TCANTIGEN.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Glycoprotein; Immune response; Immunoglobulin domain; Lipoprotein;
KW Palmitate; Repeat; Signal; T-cell; Transmembrane.
FT SIGNAL 1 25
FT CHAIN 26 458 T-cell surface glycoprotein CD4.
FT DOMAIN 26 396 Extracellular (Potential).
FT TRANSMEM 397 418 Potential.
FT DOMAIN 419 458 Cytoplasmic (Potential).
FT DOMAIN 26 125 Ig-like V-type.
FT DOMAIN 126 203 Ig-like C2-type 1.
FT DOMAIN 204 317 Ig-like C2-type 2.
FT DOMAIN 318 374 Ig-like C2-type 3.
FT CARBOHYD 296 296 N-linked (GlcNAc... ) (By similarity).
FT CARBOHYD 325 325 N-linked (GlcNAc... ) (By similarity).
FT DISULFID 41 109 By similarity.
FT DISULFID 155 184 By similarity.
FT DISULFID 328 370 By similarity.
FT LIPID 419 419 S-palmitoyl cysteine (By similarity).
FT LIPID 422 422 S-palmitoyl cysteine (By similarity).
FT CONFLICT 42 42 L -> S (in Ref. 1).
FT CONFLICT 62 62 L -> S (in Ref. 3).
FT CONFLICT 67 67 L -> S (in Ref. 2).
FT CONFLICT 169 169 K -> N (in Ref. 2).
FT CONFLICT 191 191 K -> N (in Ref. 3).
FT CONFLICT 248 248 S -> P (in Ref. 2).
FT CONFLICT 265 265 R -> Q (in Ref. 2).
FT CONFLICT 349 349 A -> T (in Ref. 2).
SQ SEQUENCE 458 AA; 50884 MW; 8BB80339FAFEC08 CRC64;

Query Match 87.9%; Score 904; DB 1; Length 458;
Best Local Similarity 87.0%; Pred. No. 3.2e-67;
Matches 174; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 1 NMRGVPFRLLLVLTQALLPAATQGNKVVLTGKGGDVEITCTASQKSKIQPFHKNSNQIK 60
DB 1 NMRGVPFRLLLVLTQALLPAATQGNKVVLTGKGGDVEITCTASQKSKIQPFHKNSNQIK 60

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QY 61 ILGNQSFLLTKGPKSLKNDRADSRSLMDQGNFPLIKKLIKEDSDTYICEVEDQKEEYOL 120
DB 61 ILGIQGLFLTKGPKSLKNDRADSRSLMDQGNFPLIKKLIKEDSDTYICEVENKEEVEL 120
QY 121 LVFGLTANSDDTHLLQGOSLTLTLSPSSPSVOCRSRGNNIOGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDDTHLLQGOSLTLTLSPSSPSVOCRSRGNNIOGKTLVSQLELDQSG 180
QY 181 TWTCTVLOQNKVKEFKIDIV 200
DB 181 TWTCTVLOQNKVKEFKIDIV 200
QY 181 TWTCTVLOQNKVKEFKIDIV 200
DB 181 TWTCTVLOQNKVKEFKIDIV 200

RESULT 6
CD4_MACNE STANDARD; PRT; 458 AA.
ID CD4_MACNE STANDARD; PRT; 458 AA.
AC 008340; P79196;
DT 01-FEB-1995 (Rel. 31, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE T-cell surface glycoprotein CD4 precursor (T-cell surface antigen T4/Leu-3).
GN Name-CD4:
OS Macaca nemestrina (Big-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.
OC NCBI_TaxID=9545;
OX [1]
RN SEQUENCE FROM N.A.
RA Hashimoto O., Tatsumi M.;
RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
RN [2]
RN SEQUENCE OF 28-424 FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=93049640; PubMed=1425921;
RA Fomsgaard A., Hirsch V.M., Johnson P.R.;
RT Cloning and sequences of primate CD4 molecules: diversity of the cellular receptor for simian immunodeficiency virus/human immunodeficiency virus."
RT Eur. J. Immunol. 22:2973-2981(1992).
RL -1- FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.
CC -1- SUBUNIT: Associates with p56-Lck (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
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CC -----
CC EMBL; D63346; BAA09670.1; -
CC EMBL; X73325; CAA51751.1; -
DR HSPSP; P01730; IWBK.
DR GO; GO:0042101; C:T-cell receptor complex; ISS.
DR GO; GO:0015026; F:coreceptor activity; ISS.
DR GO; GO:0042289; F:MHC class II protein binding; ISS.
DR GO; GO:0006955; P:immune response; ISS.
DR GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. .; ISS.
DR GO; GO:0030217; P:T-cell differentiation; ISS.
DR GO; GO:0045058; P:T-cell selection; ISS.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; ISS.
DR InterPro; IPR008424; CD2.
DR InterPro; IPR000973; CD4_TcAg.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_2.
DR PRINTS; PR00692; CD4TCANTIGEN.

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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_Like; 1.
KW Glycoprotein; Immune response; Immunoglobulin domain; Lipoprotein;
KW Palmitate; Repeat; Signal; T-cell; Transmembrane.
FT SIGNAL 1 25
FT CHAIN 26 458
FT DOMAIN 26 396
FT TRANSMEM 397 418
FT DOMAIN 419 458
FT DOMAIN 26 125
FT DOMAIN 126 203
FT DOMAIN 204 317
FT DOMAIN 318 374
FT CARBOHYD 42 42
FT CARBOHYD 296 296
FT CARBOHYD 325 325
FT DISULFID 41 109
FT DISULFID 155 184
FT DISULFID 328 370
FT LIPID 419 419
FT LIPID 422 422
FT CONFLICT 57 57
FT CONFLICT 91 91
FT CONFLICT 105 105
FT CONFLICT 113 113
FT CONFLICT 302 302
FT CONFLICT 349 349
SQ SEQUENCE 458 AA; 50905 MW; 751A9BA2C8B3EE16 CRC64;

Query Match 87.8%; Score 903; DB 1; Length 458;
Best Local Similarity 87.0%; Pred. No. 3.8e-67;
Matches 174; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

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QY 1 MNRGVPFRLHLVLTALLPATQGNKVLGKKGDVLELTCTASQKKSIGPHMKNNOIK 60
DB 1 MNRGVPFRLHLVLTALLPATQGNKVLGKKGDVLELTCTASQKKSIGPHMKNNOIK 60
QY 61 ILGNQSFLLTKGPKSLKNDRADSRSLMDQGNFPLIKKLIKEDSDTYICEVEDQKEEYOL 120
DB 61 ILGIQGLFLTKGPKSLKNDRADSRSLMDQGNFPLIKKLIKEDSDTYICEVENKEEVEL 120
QY 121 LVFGLTANSDDTHLLQGOSLTLTLSPSSPSVOCRSRGNNIOGKTLVSQLELDQSG 180
DB 121 LVFGLTANSDDTHLLQGOSLTLTLSPSSPSVOCRSRGNNIOGKTLVSQLELDQSG 180
QY 181 TWTCTVLOQNKVKEFKIDIV 200
DB 181 TWTCTVLOQNKVKEFKIDIV 200
QY 181 TWTCTVLOQNKVKEFKIDIV 200
DB 181 TWTCTVLOQNKVKEFKIDIV 200

RESULT 7
CD4_CERAE STANDARD; PRT; 458 AA.
ID CD4_CERAE STANDARD; PRT; 458 AA.
AC 008338; 002805; 077593; 028217;
DT 01-FEB-1995 (Rel. 31, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE T-cell surface glycoprotein CD4 precursor (T-cell surface antigen T4/Leu-3).
GN Name-CD4;
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Cercopithecus.
OC NCBI_TaxID=9534;
RN [1]
RN SEQUENCE FROM N.A.
RA Hashimoto O., Tatsumi M.;
RL Submitted (JUL-1996) to the EMBL/Genbank/DBJ databases.
RN [2]
RN SEQUENCE OF 28-424 FROM N.A.
RC TISSUE=Blood;

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RX MEDLINE=93049640; PubMed=1425921;
 RA Fomsgaard A., Hirsch V.M., Johnson P.R.;
 RT "Cloning and sequences of primate CD4 molecules: diversity of the
 RT cellular receptor for simian immunodeficiency virus/human
 RT immunodeficiency virus.";
 RL Eur. J. Immunol. 22:2973-2981(1992).
 RN (3)
 RP SEQUENCE OF 28-424 FROM N.A.
 RC TISSUE=Peripheral blood;
 RX MEDLINE=98017879; PubMed=9379478;
 RA Fomsgaard A., Mueller-Trutwin M.C., Diop O., Hansen J., Machiet C.,
 RA Corbet S., Barre-Sinoussi F., Allan J.S.;
 RT "Relation between phylogeny of African green monkey CD4 genes and
 RT their respective simian immunodeficiency virus genes.";
 RL J. Med. Primatol. 26:120-126(1997).
 RN [4]
 RP SEQUENCE OF 107-192 FROM N.A.
 RX MEDLINE=98320644; PubMed=9656488;
 RA Harris B.E., Diocell T.R.;
 RT "Nuclear gene trees and the phylogenetic relationships of the
 RT mangabeys (Primates: Papionini).";
 RL Mol. Biol. Evol. 15:892-900(1998).
 CC -1- FUNCTION: Accessory protein for MHC class-II antigen/T-cell
 CC receptor interaction. May regulate T-cell activation.
 CC -1- SUBUNIT: Associates with p56-lck (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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 CC -----
 DR EMBL; DB6589; BAA13132.1; -;
 DR EMBL; X73332; CA51748.1; -;
 DR EMBL; AF001226; AAB60873.1; -;
 DR EMBL; AF001228; AAB60875.1; -;
 DR EMBL; AF057380; AAC25124.1; -;
 DR HSSP; P01730; 1MIQ.
 DR GO; GO:0042101; C-T-cell receptor complex; ISS.
 DR GO; GO:0015026; F-coreceptor activity; ISS.
 DR GO; GO:0042289; F-MHC class II protein binding; ISS.
 DR GO; GO:0006955; P-immune response; ISS.
 DR GO; GO:0045086; P-positive regulation of interleukin-2 biosyn. . .; ISS.
 DR GO; GO:0030217; P-T-cell differentiation; ISS.
 DR GO; GO:0045058; P-T-cell selection; ISS.
 DR GO; GO:0007169; P-transmembrane receptor protein tyrosine kin. . .; ISS.
 DR InterPro; IPR008424; CD2.
 DR InterPro; IPR000973; CD4_TCRG.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig_2.
 DR PRINTS; PR00692; CD4TCANTIGN.
 DR PROSITE; PS50835; IG_LIKE_1.
 KW glycoprotein; immune response; Immunoglobulin domain; lipoprotein;
 KW Palmitate; Repeat; Signal; T-cell; Transmembrane.
 FT SIGNAL 1 25
 FT CHAIN 26 458
 FT DOMAIN 26 396
 FT TRANSMEM 397 418
 FT DOMAIN 419 458
 FT DOMAIN 26 125
 FT DOMAIN 126 203
 FT DOMAIN 204 317
 FT DOMAIN 318 374
 FT CARBOHYD 42 42
 FT CARBOHYD 281 281
 FT CARBOHYD 296 296
 FT CARBOHYD 325 325
 FT DISULFID 41 109
 By similarity.
 T-cell surface glycoprotein CD4.
 Extracellular (Potential).
 Potential.
 Cytoplasmic (Potential).
 Ig-like V-type.
 Ig-like C2-type 1.
 Ig-like C2-type 2.
 Ig-like C2-type 3.
 N-linked (GlcNAc. . .) (Potential).
 N-linked (GlcNAc. . .) (Potential).
 N-linked (GlcNAc. . .) (Potential).
 N-linked (GlcNAc. . .) (Potential).
 By similarity.

FT DISULFID 155 184 By similarity.
 FT DISULFID 328 370 By similarity.
 FT LIPID 419 419 S-palmitoyl cysteine (By similarity).
 FT LIPID 422 422 S-palmitoyl cysteine (By similarity).
 FT CONFLICT 46 46 K -> N (in Ref. 2 and 3; AAB60875).
 FT CONFLICT 59 59 K -> N (in Ref. 2 and 3; AAB60875).
 FT CONFLICT 115 115 G -> V (in Ref. 1).
 FT CONFLICT 165 165 G -> V (in Ref. 3; AAB60873 and 4).
 FT CONFLICT 200 200 M -> V (in Ref. 2 and 3).
 FT CONFLICT 227 227 F -> L (in Ref. 3; AAB60873).
 FT CONFLICT 271 271 K -> E (in Ref. 3; AAB60873).
 FT CONFLICT 281 281 N -> H (in Ref. 3; AAB60873).
 SQ SEQUENCE 458 AA; 51158 MW; FC523D2EDDIF72E7 CRC64;
 Query Match 86.0%; Score 885; DB 1; Length 458;
 Best Local Similarity 85.5%; Pred. No. 1,2e-65;
 Matches 171; Conservative 12; Mismatches 17; Indels 0; Gaps 0;
 QY 1 MNRGVPFRHLLVQLALPAATQGNKRVYLGKKGDTVEITCTASQKKSIOFHKNSNQIK 60
 DB 1 MMNGIFRHLVLVQLALPAATQGNKRVYLGKKGDTVEITCTASQKKSIOFHKNSNQIK 60
 QY 61 ILGNQSPFLTKGPKSLNDRADSRSLMDQNEPLIKNLKIEDSDTYICEVEDQKEEVOI 120
 DB 61 ILGNQSPFLTKGPKSLNDRADSRSLMDQNEPLIKNLKIEDSDTYICEVEDQKEEVOI 120
 QY 121 LVFGLTANSDTHLLQGSLLTLTLESPGSSPSVQCSPPGKNIQGGKTLVSQLEIDSG 180
 DB 121 LVFGLTANSDTHLLQGSLLTLTLESPGSSPSVQCSPPGKNIQGGKTLVSQLEIDSG 180
 QY 181 TWTCVQLNQKVEPKIDIV 200
 DB 181 TWTCVQLNQKVEPKIDIV 200
 QY 181 TWTCVQLNQKVEPKIDIV 200
 DB 181 TWTCVQLNQKVEPKIDIV 200
 RESULT 8
 CD4_CERTO
 ID CD4_CERTO STANDARD; PRT; 397 AA.
 AC 008536;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE T-cell surface glycoprotein CD4 (T-cell surface antigen T4/Leu-3)
 DE (Fragment).
 GN Name=CD4;
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Cercopithecidae;
 OC NCBI_Taxid=9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=93049640; PubMed=1425921;
 RA Fomsgaard A., Hirsch V.M., Johnson P.R.;
 RT "Cloning and sequences of primate CD4 molecules: diversity of the
 RT cellular receptor for simian immunodeficiency virus/human
 RT immunodeficiency virus.";
 RL Eur. J. Immunol. 22:2973-2981(1992).
 CC -1- FUNCTION: Accessory protein for MHC class-II antigen/T-cell
 CC receptor interaction. May regulate T-cell activation.
 CC -1- SUBUNIT: Associates with p56-lck (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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 CC or send an email to license@isb-sib.ch).


```

CC EMBL: X73328; CAA51754.1; -.
DR EMBL: X73327; CAA51753.1; -.
DR HSSP: P01730; IM10.
DR GO: GO:0042101; C:T-cell receptor complex; ISS.
DR GO: GO:0015026; F:coreceptor activity; ISS.
DR GO: GO:0042289; F:MHC class II protein binding; ISS.
DR GO: GO:0006955; P:immune response; ISS.
DR GO: GO:0045086; P:positive regulation of interleukin-2 biosyn. . .; ISS.
DR GO: GO:0030217; P:T-cell differentiation; ISS.
DR GO: GO:0045058; P:T-cell selection; ISS.
DR GO: GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; ISS.
DR InterPro: IPR008424; CD2_TCSG.
DR InterPro: IPR009773; CD4_TCSG.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_2.
DR PRINTS: PR00692; CD4TCANTIGEN.
DR SMART: SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE_1.
KW Glycoprotein; Immune response; Immunoglobulin domain; Lipoprotein;
KW Palmitate; Repeat; T-cell; Transmembrane.
FT NON_TER 1 369 Extracellular (Potential).
FT DOMAIN 1 370 Potential.
FT TRANSMEM 370 391 Cytoplasmic (Potential).
FT DOMAIN 392 >397 Ig-like V-type.
FT DOMAIN 392 397 Ig-like C2-type 1.
FT DOMAIN 392 397 Ig-like C2-type 2.
FT DOMAIN 392 397 Ig-like C2-type 3.
FT CARBOHYD 269 298 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 269 298 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 269 298 N-linked (GlcNAc. . .) (Potential).
FT DISULFID 14 82 By similarity.
FT DISULFID 128 157 By similarity.
FT DISULFID 301 343 S-palmitoyl cysteine (By similarity).
FT LIPID 392 392 S-palmitoyl cysteine (By similarity).
FT LIPID 395 395 Missing.
FT VARIANT 20 20 T -> I.
FT VARIANT 43 43 T -> I.
FT VARIANT 86 86 N -> D.
FT VARIANT 96 96 F -> L.
FT VARIANT 173 173 V -> M.
FT VARIANT 316 316 R -> K.
FT NON_TER 397 397
SQ SEQUENCE 397 AA; 43926 MW; 8660B636D2DB38A7 CRC64;

Query Match 76.2%; Score 784; DB 1; Length 397;
Best Local Similarity 87.3%; Pred. No. 2.9e-57;
Matches 151; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

```

```

GN Name=CD4;
OS Erythrocybus patas (Red guenon) (Cercopithecus patas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Erythrocybus.
OC NCBI_TaxID=9538;
RN [1];
RP SOURCE FROM N.A.
RC TISSUE=Blood;
RA MEDLINE=93049640; PubMed=1425921;
RA Fomsgaard A., Hirsch V.M., Johnson P.R.,
RT "Cloning and sequences of primate CD4 molecules: diversity of the
RT cellular receptor for simian immunodeficiency virus/human
RT immunodeficiency virus.";
RL Eur. J. Immunol. 22:2973-2981 (1992).
CC -1- FUNCTION: Accessory protein for MHC class-II antigen/T-cell
CC receptor interaction. May regulate T-cell activation.
CC -1- SUBUNIT: Associates with p56-lck (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X73324; CAA51750.1; -.
DR HSSP: P01730; IM10.
DR GO: GO:0042101; C:T-cell receptor complex; ISS.
DR GO: GO:0015026; F:coreceptor activity; ISS.
DR GO: GO:0042289; F:MHC class II protein binding; ISS.
DR GO: GO:0045058; P:immune response; ISS.
DR GO: GO:0045086; P:positive regulation of interleukin-2 biosyn. . .; ISS.
DR GO: GO:0030217; P:T-cell differentiation; ISS.
DR GO: GO:0045058; P:T-cell selection; ISS.
DR GO: GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; ISS.
DR InterPro: IPR008424; CD2.
DR InterPro: IPR009773; CD4_TCSG.
DR InterPro: IPR007110; Ig_Like.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_2.
DR PRINTS: PR00692; CD4TCANTIGEN.
DR SMART: SM00406; IGV_1.
DR PROSITE; PS50835; IG_LIKE_1.
KW Glycoprotein; Immune response; Immunoglobulin domain; Lipoprotein;
KW Palmitate; Repeat; T-cell; Transmembrane.
FT NON_TER 1 369 Extracellular (Potential).
FT DOMAIN 1 370 Potential.
FT TRANSMEM 370 391 Cytoplasmic (Potential).
FT DOMAIN 392 >397 Ig-like V-type.
FT DOMAIN 392 397 Ig-like C2-type 1.
FT DOMAIN 392 397 Ig-like C2-type 2.
FT DOMAIN 392 397 Ig-like C2-type 3.
FT CARBOHYD 269 298 N-linked (GlcNAc. . .) (By similarity).
FT CARBOHYD 269 298 N-linked (GlcNAc. . .) (By similarity).
FT DISULFID 14 82 By similarity.
FT DISULFID 128 157 By similarity.
FT DISULFID 301 343 By similarity.
FT DISULFID 392 392 S-palmitoyl cysteine (By similarity).
FT LIPID 395 395 S-palmitoyl cysteine (By similarity).
FT NON_TER 397 397
SQ SEQUENCE 397 AA; 44081 MW; 67887397A6B7EA4F CRC64;

Query Match 76.1%; Score 783; DB 1; Length 397;
Best Local Similarity 86.7%; Pred. No. 3.5e-57;
Matches 150; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

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Db      1 VVLGKGGDTVELTCNSQKTTQFHWKNSNQIKLGQSGFLTKGPKLDRDRSRSLW 60
Qy      88 DQGNFPLIITKMLKIEBDSYICVEVDQKEVOLLVFGLTANSPTHLQGGSLTLTLESPP 147
Db      61 DQCFSMIITKMLKIEBSEYICVEVDKKEVELLVFGLTANSPTHLQGGSLTLTLESPP 120
Qy      148 GSSPSVQCRSPRGKNIQGGKTLVSQLELDGSGTWTCTVLQNKQVEFKIDIV 200
Db      121 GSSPSVQCRSPRGKNIQGGKTLVSQLELDGSGTWTCTVLQNKQVEFKIDIV 173

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RESULT 10

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ID      009261      PRELIMINARY;      PRT;      397 AA.
AC      009261;
DT      01-JUL-1997 (TEMBLrel. 04, Created)
DT      01-JUL-1997 (TEMBLrel. 04, Last sequence update)
DT      01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE      CD4 (Fragment).
GN      Name=CD4;
OS      Cercopithecus sabaenus.
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC      Cercopithecinae; Cercopithecus.
OX      NCBI_TaxID=60711;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98017879; PubMed=9379478;
RA      Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,
RA      Corbet S., Barre-Sinoussi F., Allan J.S.;
RT      "Relation between phylogeny of African green monkey CD4 genes and
RT      their respective simian immunodeficiency virus genes.";
RL      J. Med. Primatol. 26:120-128(1997).
DR      EMBL; AF001225; AAB60872.1; -.
DR      HSSP; P01730; 1WIO.
DR      GO; GO:0016021; C:integral to membrane; IEA.
DR      GO; GO:0007155; P:cell adhesion; IEA.
DR      GO; GO:0006955; P:immune response; IEA.
DR      InterPro; IPR008424; CD2.
DR      InterPro; IPR000973; CD4_TcAg.
DR      InterPro; IPR007110; Ig_Like.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF05790; C2-sect. 2.
DR      Pfam; PF00047; Ig_1.
DR      PRINTS; PR00692; CD4TCANTIGEN.
DR      SMART; SM00406; IGV_1.
DR      PROSITE; PSS0835; IG_LIKE; 1.
FT      NON_TER      1
FT      NON_TER      397
SQ      SEQUENCE      397 AA; 43945 MW; 80C963B92A868CD3 CRC64;

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Query Match 74.5%; Score 767; DB 2; Length 397;
 Best local Similarity 85.5%; Pred. No. 7.6e-56;
 Matches 148; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

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Qy      28 VVLGKGGDTVELTCNSQKSIQFHWKNSNQIKLGQSGFLTKGPKLDRDRSRSLW 87
Db      1 VVLGKGGDTVELTCNSQNTTQFHWKNSNQIKLGQSGFLTKGSKLDRDRSRSLW 60
Qy      88 DQGNFPLIITKMLKIEBDSYICVEVDQKEVOLLVFGLTANSPTHLQGGSLTLTLESPP 147
Db      61 DQCFSMIITKMLKIEBSEYICVEVDKKEVELLVFGLTANSPTHLQGGSLTLTLESPP 120
Qy      148 GSSPSVQCRSPRGKNIQGGKTLVSQLELDGSGTWTCTVLQNKQVEFKIDIV 200
Db      121 GSSPSVQCRSPRGKNIQGGKTLVSQLELDGSGTWTCTVLQNKQVEFKIDIV 173

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RESULT 11
 009262
 ID 009262; PRELIMINARY; PRT; 397 AA.
 AC 009262;

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DT      01-JUL-1997 (TEMBLrel. 04, Created)
DT      01-JUL-1997 (TEMBLrel. 04, Last sequence update)
DT      01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE      CD4 (Fragment).
GN      Name=CD4;
OS      Cercopithecus tanzanus.
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC      Cercopithecinae; Cercopithecus.
OX      NCBI_TaxID=60712;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98017879; PubMed=9379478;
RA      Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,
RA      Corbet S., Barre-Sinoussi F., Allan J.S.;
RT      "Relation between phylogeny of African green monkey CD4 genes and
RT      their respective simian immunodeficiency virus genes.";
RL      J. Med. Primatol. 26:120-128(1997).
DR      EMBL; AF001221; AAB60868.1; -.
DR      HSSP; P01730; 1WIO.
DR      GO; GO:0016021; C:integral to membrane; IEA.
DR      GO; GO:0007155; P:cell adhesion; IEA.
DR      GO; GO:0006955; P:immune response; IEA.
DR      InterPro; IPR008424; CD2.
DR      InterPro; IPR000973; CD4_TcAg.
DR      InterPro; IPR007110; Ig_Like.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF05790; C2-sect. 2.
DR      Pfam; PF00047; Ig_1.
DR      PRINTS; PR00692; CD4TCANTIGEN.
DR      SMART; SM00406; IGV_1.
DR      PROSITE; PSS0835; IG_LIKE; 1.
FT      NON_TER      1
FT      NON_TER      397
SQ      SEQUENCE      397 AA; 43954 MW; CF7F2F5D8233580D CRC64;

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Query Match 74.5%; Score 767; DB 2; Length 397;
 Best local Similarity 85.5%; Pred. No. 7.6e-56;
 Matches 148; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

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Qy      28 VVLGKGGDTVELTCNSQKSIQFHWKNSNQIKLGQSGFLTKGPKLDRDRSRSLW 87
Db      1 VVLGKGGDTVELTCNSQNTTQFHWKNSNQIKLGQSGFLTKGSKLDRDRSRSLW 60
Qy      88 DQGNFPLIITKMLKIEBDSYICVEVDQKEVOLLVFGLTANSPTHLQGGSLTLTLESPP 147
Db      61 DQCFSMIITKMLKIEBSEYICVEVDKKEVELLVFGLTANSPTHLQGGSLTLTLESPP 120
Qy      148 GSSPSVQCRSPRGKNIQGGKTLVSQLELDGSGTWTCTVLQNKQVEFKIDIV 200
Db      121 GSSPSVQCRSPRGKNIQGGKTLVSQLELDGSGTWTCTVLQNKQVEFKIDIV 173

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RESULT 12
 009263
 ID 009263; PRELIMINARY; PRT; 397 AA.
 AC 009263;
 DT 01-JUL-1997 (TEMBLrel. 04, Created)
 DT 01-JUL-1997 (TEMBLrel. 04, Last sequence update)
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE CD4 (Fragment).
 GN Name=CD4;
 OS Cercopithecus tanzanus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=60712;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98017879; PubMed=9379478;
 RA Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,
 RA Corbet S., Barre-Sinoussi F., Allan J.S.;
 RT "Relation between phylogeny of African green monkey CD4 genes and

RT their respective simian immunodeficiency virus genes.";
RL J. Med. Primatol. 26:120-128(1997).
DR EMBL; AF001222; AAB60868.1; -.
DR HSSP; P01730; IMIO.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0007155; P: cell adhesion; IEA.
DR GO; GO:0006955; P: immune response; IEA.
DR InterPro; IPR008424; CD2.
DR InterPro; IPR009713; CD4_TcAg.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF05790; C2-set; 2.
DR PRINTS; PR00692; CD4TCANTIGEN.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 397 AA; 43994 MW; A3CD031535A51524 CRC64;

Query Match 74.5%; Score 767; DB 2; Length 397;
Best Local Similarity 85.5%; Pred. No. 7.6e-56;
Matches 148; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 28 VVLGKKGDVVELTCTASQKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADRSRLW 87
DB 1 VVLGKKGDVVELTCTASQKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADRSRLW 60
QY 88 DQGNPFLIKNLKIEDSDTYICEVEDQKEVQLVFGLTANSDPHTLQGSFLTLTLESPP 147
DB 61 DQGFSPMIITKNLKIETSEYICVENKKEVEVLVFGLTANSDPHTLQGSFLTLTLESPP 120
QY 148 GSSPSVQCRSPRGKNIQGGKTLVSQLELQDSGTWTCVLYONQKVEFKIDIV 200
DB 121 GSSPSVQCRSPRGKNIQGGKTLVSQLELQDSGTWTCVLYONQKVEFKIDIV 173

RESULT 13
Q95NE9 PRELIMINARY; PRT; 397 AA.
AC Q95NE9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CD4 (Fragment).
GN Name=CD4;
OS Cercopithecus pygerythrus (Vervet monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
NCBI_TaxID=60710;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98017879; PubMed=9379478;
RA Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,
RT Corbet S., Barre-Sinoussi F., Allan J.S.;
RT "Relation between phylogeny of African green monkey CD4 genes and
RT their respective simian immunodeficiency virus genes.";
RL J. Med. Primatol. 26:120-128(1997).
DR EMBL; AF001227; AAB60874.1; -.
DR HSSP; P01730; IMIO.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0007155; P: cell adhesion; IEA.
DR GO; GO:0006955; P: immune response; IEA.
DR InterPro; IPR008424; CD2.
DR InterPro; IPR009713; CD4_TcAg.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF05790; C2-set; 2.
DR Pfam; PF00047; Ig; 1.
DR PRINTS; PR00692; CD4TCANTIGEN.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.

FT NON_TER 1
FT NON_TER 397
SQ SEQUENCE 397 AA; 43946 MW; 21C3E30882ABFC0 CRC64;

Query Match 74.5%; Score 767; DB 2; Length 397;
Best Local Similarity 85.5%; Pred. No. 7.6e-56;
Matches 148; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 28 VVLGKKGDVVELTCTASQKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADRSRLW 87
DB 1 VVLGKKGDVVELTCTASQKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADRSRLW 60
QY 88 DQGNPFLIKNLKIEDSDTYICEVEDQKEVQLVFGLTANSDPHTLQGSFLTLTLESPP 147
DB 61 DQGFSPMIITKNLKIETSEYICVENKKEVEVLVFGLTANSDPHTLQGSFLTLTLESPP 120
QY 148 GSSPSVQCRSPRGKNIQGGKTLVSQLELQDSGTWTCVLYONQKVEFKIDIV 200
DB 121 GSSPSVQCRSPRGKNIQGGKTLVSQLELQDSGTWTCVLYONQKVEFKIDIV 173

RESULT 14
O09259 PRELIMINARY; PRT; 397 AA.
AC O09259;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CD4 (Fragment).
GN Name=CD4;
OS Cercopithecus sabaues.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
NCBI_TaxID=60711;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98017879; PubMed=9379478;
RA Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,
RT Corbet S., Barre-Sinoussi F., Allan J.S.;
RT "Relation between phylogeny of African green monkey CD4 genes and
RT their respective simian immunodeficiency virus genes.";
RL J. Med. Primatol. 26:120-128(1997).
DR EMBL; AF001223; AAB60870.1; -.
DR HSSP; P01730; IMIO.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0007155; P: cell adhesion; IEA.
DR GO; GO:0006955; P: immune response; IEA.
DR InterPro; IPR008424; CD2.
DR InterPro; IPR009713; CD4_TcAg.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF05790; C2-set; 2.
DR Pfam; PF00047; Ig; 1.
DR PRINTS; PR00692; CD4TCANTIGEN.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 397
SQ SEQUENCE 397 AA; 43861 MW; 7CE39AD0F8506C81 CRC64;

Query Match 74.1%; Score 763; DB 2; Length 397;
Best Local Similarity 85.0%; Pred. No. 1.7e-55;
Matches 147; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 28 VVLGKKGDVVELTCTASQKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADRSRLW 87
DB 1 VVLGKKGDVVELTCTASQKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADRSRLW 60
QY 88 DQGNPFLIKNLKIEDSDTYICEVEDQKEVQLVFGLTANSDPHTLQGSFLTLTLESPP 147
DB 61 DQGFSPMIITKNLKIETSEYICVENKKEVEVLVFGLTANSDPHTLQGSFLTLTLESPP 120

QY 148 GSSPSVQCRSPRGKNIQGGKTLVSQLELDGSGTWTCTVLQNGKVEFKIDIV 200
DB 121 GSSPSVYKCRSPRGKNIQGGKTLVSQLELDGSGTWTCTVNSQDQNTVEFKIDIV 173

RESULT 15

ID 009260 PRELIMINARY; PRT; 397 AA.
AC 009260;
DT 01-JUL-1997 (T-EMBLrel. 04, Created)
DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE CD4 (fragment).
GN Name=CD4;
OS Cercopithecus sabaues.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=60711;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98017879; PubMed=9379478;
RA Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Machiot C.,
RA Cordet S., Barre-Sinoussi F., Allan J.S.,
RT "Relation between phylogeny of African green monkey CD4 genes and
RT their respective simian immunodeficiency virus genes."
RL J. Med. Primatol. 26:120-128(1997).
DR EMBL; AF001224; AAB60871.1; -.
DR HSSP; P01730; IWIO.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR008424; CD2.
DR InterPro; IPR007110; Ig-TcAg.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF05790; C2-sec; 2.
DR Pfam; PF00047; Ig_1.
DR PRINTS; PR00692; CD4TCANTIGEN.
DR SMART; SM00406; IGY; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 397
SQ SEQUENCE 397 AA; 43882 MW; 478BB277E992EBE89 CRC64;

Query Match 74.1%; Score 763; DB 2; Length 397;
Best Local Similarity 85.0%; Pred. No. 1.7e-55;
Matches 147; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 28 VVLGKGGDTVELTCTASOKSIQFHMKNNSQIKILGQGSFLTKGPKLNDRADSRRLW 87
DB 1 VVLGKGGDTVELTCTASOKSIQFHMKNNSQIKILGQGSFLTKGSKLNDRIDSRKSLW 60
QY 88 DQGNFPLIKNLKIEDSDTYICEVEDQKEVQLLVFGLTANSDTHLQGSQSLTTLTLESP 147
DB 61 DQCFEMITIKNLKIEDSETYICEVENKEVEVLVFGLTANSDTHLQGSQSLTTLTLESP 120
QY 148 GSSPSVQCRSPRGKNIQGGKTLVSQLELDGSGTWTCTVLQNGKVEFKIDIV 200
DB 121 GSSPSVYKCRSPRGKNIQGGKTLVSQLELDGSGTWTCTVNSQDQNTVEFKIDIV 173

Search completed: March 7, 2005, 07:19:30
Job time : 75.9095 secs

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